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(57) Abstract

Peptides of the formula (1) ^{N}TCPPCPXYCPPCPA^{C} are described wherein X and Y, which may be the same or different, is each a neutral aliphatic L-amino acid residue, and protected and reactive derivatives thereof. The peptides may be used as hinge regions in proteins, where they are capable of being covalently coupled to achieve dimeric structure, for example as found in antibodies.

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INTERNATIONAL SEARCH REPORT

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A. CLASSIFICATION OF SUBJECT MATTER
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B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
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C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	M.L. RODRIGUES ET AL.: "Engineering Fab' Fragments for Efficient F(ab)2 Formation in Escherichia coli and for Imrpobed In Vivo Stability" JOURNAL OF IMMUNOLOGY, vol. 151, no. 12, 15 December 1993, pages 6954-6961, XP002098809 BALTIMORE US cited in the application see page 6959, right-hand column, paragraph 2 --- -/--	1-8

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
P,X	HUMPHREYS, DAVID P. ET AL: "Formation of dimeric Fabs in Escherichia coli: effect of hinge size and isotype, presence of interchain disulfide bond, Fab' expression levels, tail piece sequences and growth conditions" J. IMMUNOL. METHODS (1997), 209(2), 193-202 CODEN: JIMMBG;ISSN: 0022-1759, 1 December 1997, XP004103797 see page 198, left-hand column, paragraph 2 - right-hand column, paragraph 2; table 1 ---	1-8
A	M. BETTER ET AL.: "Potent anti-CD5 ricin A chain immunoconjugates from bacterially produced Fab' and F(ab')2" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, vol. 90, no. 2, 15 January 1993, pages 457-461, XP002098811 WASHINGTON US cited in the application see figure 1 ---	1,7
A	EP 0 284 898 A (MAX PLANCK GESELLSCHAFT) 5 October 1988 see claims; examples -----	1-8

3

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INTERNATIONAL SEARCH REPORT

Information on patent family members

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Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP 0284898 A	05-10-1988	JP 63258895 A	26-10-1988
		US 5041533 A	20-08-1991

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(54) Title: PEPTIDES

(57) Abstract

Peptides of the formula (1) ^{N}TCPPCPXYCPPCPA^{C} are described wherein X and Y, which may be the same or different, is each a neutral aliphatic L–amino acid residue, and protected and reactive derivatives thereof. The peptides may be used as hinge regions in proteins, where they are capable of being covalently coupled to achieve dimeric structure, for example as found in antibodies.

^{N}TCPPCPXYCPPCPA^{C} (1)

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PEPTIDES

This invention relates to peptides which function as hinge regions in proteins, to proteins containing such hinge regions and to the use of said proteins in medicine.

In clinical antibody therapy and imaging applications the avidity of a dimeric antibody species is often required to achieve an effective antibody affinity *in vivo*, but without the effector functions or lengthy serum permanence conferred by the Fc domain (ref. 1-3 – for the literature referenced by number herein see the list "References" hereinafter). $F(ab')_2$ molecules meet this requirement and can be produced by proteolytic cleavage of monoclonal IgG of appropriate isotypes, or by use of recombinant immunoglobulin derived domains produced in *E.coli*.

The ability to secrete antibody fragments to the oxidising periplasm of *E.coli* has led to rapid advances in the engineering of grafted, highly expressed Fab's. Importantly, the use of *E.coli* also enables the cost effective and rapid production of the amounts of antibody material required to supply a large market (ref. 4, 5). Engineered Fab' is often expressed with only one hinge-cysteine. This cysteine can be used for attachment of other Fab's to make a $F(ab')_2$ or attachment of therapeutic effector molecules such as radionuclides, enzymes, or toxins (ref. 6).

Several protein engineering approaches for producing divalent antigen binding species *in vivo* in *E.coli* have been reported, using both modified scFvs and Fab's. Simple hinge modifications do not give substantial yields *in vivo* of dimeric species from *E.coli* (ref. 7-9). Techniques for increasing dimerisation *in vivo* are well characterised, but these often use large non-immunoglobulin dimerisation motifs which are potentially immunogenic and can cause severe reductions in the level of expression of soluble protein (ref. 10-13). The simplest route to production of dimeric antigen binding species remains the direct disulphide or chemical cross-linking of Fab's *in vitro* (ref. 2, 7, 14, 15). The choice of covalent linkage between the two Fab's is an important one. If the $F(ab')_2$ is cleaved *in vivo* then the resulting Fab' molecules generated suffer both from loss of avidity and very rapid clearance from the circulation (ref. 1, 2). Single disulphide bonds are known to be more susceptible to cleavage *in vivo* than protected disulphides, sulphide, or thioether bonds (ref. 2, 9, 16). However, two disulphides as found in the hinge region of $F(ab')_2$ isolated from proteolytic cleavage of IgG1 have previously been found to be as robust as one thioether bond, as judged by serum permanence (ref. 9).

There is a need for non-immunogenic dimeric antibody species which overcome the problem of facile *in vivo* cleavage while still being efficient to manufacture and couple to other effector molecules. We have now found a peptide, which when part of a larger protein such as a Fab' fragment efficiently generates dimers and yields dimeric material which is highly resistant to chemical reduction *in vitro* and has long serum permanence times *in vivo*. Advantageously, the peptide is well tolerated in *E.coli* and in our tests to date has been shown to be non-immunogenic.

Thus according to one aspect of the invention we provide a peptide of formula (1):

$$^{N}TCPPCPXYCPPCPA^{C} \quad (1)$$

wherein X and Y, which may be the same or different, is each a neutral aliphatic L-amino acid residue, and protected and reactive derivatives thereof.

In formula (1) and the other peptides described herein conventional single letter abbreviations are used to represent amino acid residues except where otherwise indicated. The superscripts "N" or "C" are used to indicate respectively the N- or C-terminal residue of a peptide.

Neutral L-amino acid residues represented by each of the groups X and Y include glycine, alanine, valine, leucine, isoleucine, serine and threonine residues.

Protected derivatives of the peptides of formula (1) include N- and C-terminal protected derivatives in which the N-terminal amino group or the C-terminal carboxyl group is linked to a protecting group. N-protected derivatives include for example optionally substituted benzyloxy-carbonylamino, allyloxycarbonylamino, cycloalkyloxycarbonylamino, t-butoxycarbonylamino, trifluoroacetylamino, phthalylamino, aralkylamino, e.g. benzylamino, diphenylmethylamino or triphenylmethylamino, tosyl-amino or formylamino derivatives. C-protected derivatives include for example esters, such as optionally substituted alkyl, e.g. methyl, ethyl or t-butyl, aralkyl, e.g. benzyl or benzhydryl, silyl, e.g. trimethylsilyl and phthalimidomethyl esters, and esters with polymers, for example functionalised styrene-based resins.

Reactive derivatives of peptides of formula (1) include those in which the C-terminal carboxyl group is functionalised, and is, for example, an acyl halide such as an acyl chloride, an acyl cyanide or azide, an anhydride, an ester, for example a N-hydroxy

succinimide, p-nitrophenyl or pentachloro-phenyl ester, a N-acyl heterocycle such as a N-acyl imidazole, pyrazole or triazole or an activated acid formed by addition of a carbodiimide or isoxazolium reagent.

Particularly useful peptides of formula (1) include those wherein X is an alanine residue. In another preference, Y in particular is a threonine residue. An especially useful peptide according to the invention has the formula (2):

$$^{N}TCPPCPATCPPCPA^{C} \quad (2)$$

and protected and reactive derivatives thereof.

The peptides according to the invention may be prepared from appropriately activated and/or protected amino acids [for example utilising reactive derivatives and protecting groups of the types mentioned in connection with the peptides of formula (1)] using routine peptide synthesis techniques [see for example Merrifield, B. Science (1985), 232, 341-347].

The presence of four cysteine residues in each peptide of formula (1) provides four centres for disulphide and/or thioether bond formation thus allowing reaction with other molecules containing thiol reactive groups. In particular dimeric proteins may be obtained by incorporating the peptides in protein chains and the invention extends to such a use. In order to achieve protein dimerisation a peptide of formula (1) must first be coupled to an existing protein chain or synthesised *de novo* as part of it and we therefore provide in another aspect of the invention a protein comprising one polypeptide chain characterised in that said chain contains an amino acid sequence $^{N}TCPPCPXYCPPCPA^{C}$, wherein X and Y are as defined for the peptide of formula (1).

The invention also extends to proteins containing two polypeptide chains covalently linked via the cysteine residues in $^{N}TCPPCPXYCPPCPA^{C}$ as explained above and thus according to a further aspect of the invention we provide a protein comprising two polypeptide chains characterised in that each of said chains contains an amino acid sequence $^{N}TCPPCPXYCPPCPA^{C}$ [wherein X and Y are as defined for the peptide of formula (1)] and each chain is covalently linked to the other through one, two, three or four of the cysteine residues present in each of said amino acid sequences.

In the proteins according to the invention the amino acid sequence ^{N}TCPPCPXYCPPCPA^{C} is preferably a sequence ^{N}TCPPCPAYCPPCPA^{C} or ^{N}TCPPCPXTCPPCPA^{C}, especially the sequence ^{N}TCPPCPATCPPCPA^{C}.

The proteins according to the invention may be naturally occurring proteins to which the peptide of formula (1) has been coupled, or recombinant proteins incorporating the amino acid sequence ^{N}TCPPCPXYCPPCPA^{C}. The proteins may generally be structural or, especially, binding proteins. Particular binding proteins include hormones, cytokines, colony stimulating factors, growth factors, releasing factors, ion carriers, toxins, and receptors thereof, including all or part of receptors associated with binding to cell surface associated molecules, the T-cell receptor, CD4, CD8, CD28, cytokine receptors, e.g. an interleukin receptor, TNF receptor or interferon receptor, receptors for colony stimulating factors e.g. G-CSF or GM-CSF, platelet derived growth factors e.g. PDGF-α and PDGF-β, and in particular antibodies and antigen binding fragments thereof.

Where the protein according to the invention has one peptide chain containing a ^{N}TCPPCPXYCPPCPA^{C} amino acid sequence it may be a monomeric protein or be separately linked to one or more other polypeptide chains to form overall a multimeric structure. In those proteins of the invention containing two polypeptide chains with covalently linked ^{N}TCPPCPXYPPCPA^{C} sequences the protein will clearly be at least dimeric but may also consist of other, separately linked chains to form overall a multimeric structure. Dimers and multimers may be composed of more than one type of polypeptide chain and may be homo- or heteromeric.

The production of proteins according to the invention may be achieved using standard chemical or recombinant DNA techniques. Chemical techniques include chemical coupling of a protein and a peptide of formula (1) using activated and protected derivatives of the protein and peptide as described above in relation to the production of peptides of formula (1). In this way, for example, a peptide of formula (1) may be site-specifically coupled to the C-terminal end of a suitably C-activated protein.

Recombinant DNA techniques generally involve the expression of a protein by a host cell, followed by recovery of the protein using standard separation and purification techniques. DNA coding for the protein may be introduced into any suitable expression vector by operatively linking the DNA to any necessary expression control elements therein and transforming any suitable procaryotic or eucaryotic host cell

with the vector using well known procedures. A more detailed description of suitable techniques is given hereinafter in relation to the production of antibodies according to the invention. These may be generally followed and/or easily adapted to enable the production of any protein according to the invention by recombinant means. The use of recombinant DNA technology provides a flexible approach to proteins according to the invention in that it enables the easy manipulation and insertion of a peptide of formula (1) at any desired position in a protein. DNA coding for a peptide of formula (1) is thus particularly useful and forms a further aspect of the invention. DNA containing the following nucleotide sequence:

5' ACATGCCCGCCGTGCCCGGCGACCTGCCCGCCGTGCCCGGCG 3'

[where each letter is the standard code for a nucleotide] coding for the amino acid sequence ^{N}TCPPCPATCPPCA^{C} is especially useful and the invention extends to DNA comprising this sequence together with variants thereof wherein one or more nucleotides have been substituted due to the degeneracy of the genetic code. The invention also extends to recombinant plasmids containing DNA coding for a peptide of formula (1), to cells containing said plasmids and to a process for producing a protein according to the invention which comprises culturing said cells such that the desired protein is expressed and recovering the protein from the culture

The amino acid sequences ^{N}TCPPCPXYCPPCPA^{C} are particularly suitable for use with binding proteins such as cell-associated receptors or antibodies where each sequence can function as a hinge region to provide a dimerisation capacity. Thus, for example, recombinant receptors [see for example International Patent Specifications Nos. WO 92/100591, WO 92/15322, WO 93/19163, WO 95/02686 and WO 97/23613] can be designed which incorporate these sequences to facilate dimerisation of the individual receptor chains required for efficient receptor binding and the invention extends to a recombinant receptor comprising at least one peptide of formula (1). Such receptors are of use for example to redirect and activate cells [see the patent specifications just mentioned] and the invention includes such cells expressing a recombinant receptor comprising at least one peptide of formula (1).

In antibodies the sequences ^{N}TCPPCPXYCPPCPA^{C} can be used as substitutes for naturally occurring hinge regions [the hinge region is located between the C_H1 and C_H2 domains in naturally occurring immunoglobulins]. The sequences are particularly suited for this purpose and in a preferred aspect of the invention we provide an antibody containing a hinge region characterised in that said hinge region has an amino acid sequence ^{N}TCPPCPXYCPPCPA^{C} where X and

Y are as defined for formula (1). In this instance, the hinge region preferably has an amino acid sequence ^{N}TCPPCPAYCPPCPA^{C} or ^{N}TCPPCPXTCPPCPA^{C}, more especially ^{N}TCPPCATCPPCPA^{C}.

The term "antibody" as used herein is generally intended to include monovalent, divalent or other multivalent antibodies. Thus for example a monovalent antibody according to the invention may be a single chain comprising an immunoglobulin heavy chain variable (V_H) domain and a ^{N}TCPPCPXYCPPCPA^{C} hinge region directly attached to it, preferably at the C-terminal end of the V_H domain. Alternatively, the V_H domain and hinge region may be separated by a spacer region comprising one or more amino acids in peptide linkage to each other and the rest of the antibody. The spacer region may be for example one or more immunoglobulin heavy (C_H) or light (C_L) chain constant domains or fragments thereof for example a C_H1 domain or a fragment thereof and/or a C_H2 and/or a C_H3 domain or fragments thereof. Where desired the hinge region may have one or more other amino acids attached to its C-terminus for example one or more immunoglobulin constant region domains or fragments thereof as just described. The V_H domain may be monomeric or it may be dimeric and contain V_H-V_H or V_H-V_L (where V_L is an immunoglobulin light chain variable domain) dimers in which the V_H and V_L chains are non-covalently associated. Where desired however, the chains may be covalently coupled either directly, for example via a disulphide bond between the two variable domains, or through a linker, for example a peptide linker, to form a single chain domain. Particular examples of monovalent antibodies according to the invention include Fv, single chain Fv and especially Fab or Fab' fragments each containing a hinge region having the sequence ^{N}TCPPCPXYCPPCPA^{C}.

Divalent antibodies according to the invention include two of the monomeric chains just described covalently linked through one, two, three or four of the cysteine residues of the hinge region ^{N}TCPPCXYCPPCPA^{C} of each chain. The linkage may be a simple disulphide linkage or may be via a linker group, for example as described in International Patent Specifications Nos. WO 90/09195 and WO 90/09196. Particular divalent antibodies include $F(ab)_2$ and $F(ab')_2$ fragments.

Multivalent antibodies according to the invention include for example tri- and tetravalent antibodies comprising three or four of the monomeric chains described above linked via their hinge regiuons by a linker, for example as described in International Patent Specification No. 92/22583.

The antibody according to the invention will in general be capable of selectively binding to an antigen. The antigen may be any cell-associated antigen, for example a cell surface antigen such as a T-cell, endothelial cell or tumour cell marker, or it may be a soluble antigen. Particular examples of cell surface antigens include adhesion molecules, such as E-selectin, P-selectin or L-selectin, CD2, CD3, CD4, CD5, CD7, CD8, CD11a, CD11b, CD18, CD19, CD20, CD23, CD25, CD33, CD38, CD40, CD45, CDW52, CD69, carcinoembryonic antigen (CEA), human milk fat globulin (HMFG1 and 2), MHC Class I and MHC Class II antigens, and VEGF, and where appropriate, receptors thereof. Soluble antigens include interleukins such as IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-8 or IL-12, viral antigens, for example respiratory syncytial virus or cytomegalovirus antigens, interferons such as interferon-α, interferon-β or interferon-γ, tumour necrosis factor-α, tumour necrosis factor-β, colony stimulating factors such as G-CSF or GM-CSF, and platelet derived growth factors such as PDGF-α, and PDGF-β and where appropriate receptors thereof.

The variable region domain(s) may be any naturally occurring variable domain or an engineered version thereof. By engineered version is meant a variable region domain which has been created using recombinant DNA engineering techniques. Such engineered versions include those created for example from natural antibody variable regions by insertions, deletions or changes in or to the amino acid sequences of the natural antibodies. Particular examples of this type include those engineered variable region domains containing at least one complementarity determining region (CDR) and optionally one or more framework amino acids from one antibody and the remainder of the variable region domain from a second antibody.

Antibodies according to the invention may be obtained from any whole antibody, especially a whole monoclonal antibody, [prepared by conventional immunisation and cell fusion procedures], using any suitable standard enzymatic cleavage and/or digestion techniques, for example by treatment with pepsin followed by chemical coupling with a peptide of formula (1) or a protected or activated derivative thereof using routine protein synthesis techniques as described above in relation to the production of peptides of formula (1). Alternatively, the antibody of the invention may be prepared by the use of recombinant DNA techniques involving the manipulation and re-expression of DNA encoding antibody variable and/or constant regions. Such DNA is known and/or is readily available from DNA libraries including for example phage-antibody libraries [see Chiswell, D. J. and McCafferty, J. Tibtech. 10 80-84 (1992)] or where desired can be synthesised. Standard molecular biology and/or

chemistry procedures may be used to sequence and manipulate the DNA, for example, to introduce codons to create a sequence ^{N}TCPPCPXYCPPCPA^{C}, to modify, add or delete other amino acids or domains as desired.

From here, one or more replicable expression vectors containing the DNA may be prepared and used to transform an appropriate cell line, e.g. a non-producing myeloma cell line, such as a mouse NSO line or a bacterial, e.g. *E.coli* line, in which production of the antibody will occur. In order to obtain efficient transcription and translation, the DNA sequence in each vector should include appropriate regulatory sequences, particularly a promoter and leader sequence operably linked to the variable domain sequence. Particular methods for producing antibodies in this way are generally well known and routinely used. For example, basic molecular biology procedures are described by Maniatis *et al* [Molecular Cloning, Cold Spring Harbor Laboratory, New York, 1989]; DNA sequencing can be performed as described in Sanger *et al* [PNAS 74, 5463, (1977)] and the Amersham International plc sequencing handbook; and site directed mutagenesis can be carried out according to the method of Kramer *et al* [Nucl. Acids Res. 12, 9441, (1984)] and the Anglian Biotechnology Ltd handbook. Additionally, there are numerous publications, including patent specifications, detailing techniques suitable for the preparation of antibodies by manipulation of DNA, creation of expression vectors and transformation of appropriate cells, for example as reviewed by Mountain A and Adair, J R in Biotechnology and Genetic Engineering Reviews [ed. Tombs, M P, 10, Chapter 1, 1992, Intercept, Andover, UK] and in International Patent Specification No. WO 91/09967. Once expressed, the antibody may be separated from the host cell and purified using standard centrifugation, filtration, chromatography and other separation/purification techniques, for example as described in the Examples hereinafter.

Antibody fragments containing a sequence ^{N}TCPPCPXYCPPCPA^{C}, particularly Fab or Fab' fragments are particularly suited for manufacture in *E.coli* as described above and in the Examples herein.

Where desired, the protein, including antibody, according to the invention may have one or more effector or reporter molecules attached to it and the invention extends to such modified proteins and, in particular, antibodies. The effector or reporter molecules may be attached to the protein through any available amino acid side-chain or terminal amino acid functional group located in the protein, for example any free amino, imino, hydroxyl or carboxyl group. In one preference however the

molecule may be attached to a cysteine residue in an amino acid sequence ^{N}TCPPCPXYCPPCPA^{C}. Dimers containing these sequences are particularly resistant to chemical reduction *in vitro* and advantageously can be partially reduced to expose reactive thiols to which effector or reporter molecules may be attached. One, two, three or more effector or reporter molecules may be attached in this way.

Effector molecules include, for example, antineoplastic agents, toxins (such as enzymatically active toxins of bacterial or plant origin and fragments thereof e.g. ricin and fragments thereof) biologically active proteins, for example enzymes, synthetic or naturally occurring polymers, nucleic acids and fragments thereof, e.g. DNA, RNA and fragments thereof, radionuclides, particularly radioiodide, and chelated metals. Suitable reporter groups include chelated metals, fluorescent compounds or compounds which may be detected by NMR or ESR spectroscopy.

Particular antineoplastic agents include cytotoxic and cytostatic agents, for example alkylating agents, such as nitrogen mustards (e.g. chlorambucil, melphalan, mechlorethamine, cyclophosphamide, or uracil mustard) and derivatives thereof, triethylenephosphoramide, triethylenethiophosphor-amide, busulphan, or cisplatin; antimetabolites, such as methotrexate, fluorouracil, floxuridine, cytarabine, mercaptopurine, thioguanine, fluoroacetic acid or fluorocitric acid, antibiotics, such as bleomycins (e.g. bleomycin sulphate), doxorubicin, daunorubicin, mitomycins (e.g. mitomycin C), actinomycins (e.g. dactinomycin) plicamycin, calichaemicin and derivatives thereof, or esperamicin and derivatives thereof; mitotic inhibitors, such as etoposide, vincristine or vinblastine and derivatives thereof; alkaloids, such as ellipticine; polyols such as taxicin-I or taxicin-II; hormones, such as androgens (e.g. dromostanolone or testolactone), progestins (e.g. megestrol acetate or medroxyprogesterone acetate), estrogens (e.g. dimethylstilbestrol diphosphate, polyestradiol phosphate or estramustine phosphate) or antiestrogens (e.g. tamoxifen); anthraquinones, such as mitoxantrone, ureas, such as hydroxyurea; hydrazines, such as procarbazine; or imidazoles, such as dacarbazine.

Synthetic or naturally occurring polymers include for example optionally substituted straight or branched chain polyalkylene, polyalkenylene or polyoxyalkylene polymers such as polyethyleneglycol, polypropylene glycol, polyvinylalcohol and especially, methoxypolyethylene glycol or branched or unbranched polysaccharides, e.g. a homo- or hetero-polysaccharide such as lactose, amylose, dextran or gylcogen.

Chelated metals include chelates of di-or tripositive metals having a coordination number from 2 to 8 inclusive. Particular examples of such metals include technetium (Tc), rhenium (Re), cobalt (Co), copper (Cu), gold (Au), silver (Ag), lead (Pb), bismuth (Bi), indium (In), gallium (Ga), yttrium (Y), terbium (Tb), gadolinium (Gd), and scandium (Sc). In general the metal is preferably a radionuclide. Particular radionuclides include ^{99m}Tc, ^{186}Re, ^{188}Re, ^{58}Co, ^{60}Co, ^{67}Cu, ^{195}Au, ^{199}Au, ^{110}Ag, ^{203}Pb, ^{206}Bi, ^{207}Bi, ^{111}In, ^{67}Ga, ^{68}Ga, ^{88}Y, ^{90}Y, ^{160}Tb, ^{153}Gd and ^{47}Sc.

The chelated metal may be for example one of the above types of metal chelated with any suitable polydentate chelating agent, for example acyclic or cyclic polyamines, polyethers, (e.g. crown ethers and derivatives thereof); polyamides; porphyrins; and carbocyclic derivatives.

In general, the type of chelating agent will depend on the metal in use. One particularly useful group of chelating agents in conjugates according to the invention, however, are acyclic and cyclic polyamines, especially polyaminocarboxylic acids, for example diethylenetriaminepentaacetic acid and derivatives thereof, and macrocyclic amines, e.g. cyclic tri-aza and tetra-aza derivatives (for example as described in International Patent Specification No. WO 92/22583); and polyamides, especially desferriox-amine and derivatives thereof.

Particularly useful effector groups are calichaemicin and derivatives thereof (see for example South African Patent Specifications Nos. 85/8794, 88/8127 and 90/2839).

Where it is desired to obtain a protein according to the invention linked to an effector or reporter molecule this may be prepared by standard chemical or recombinant DNA procedures in which the protein is linked either directly or via a coupling agent to the effector or reporter molecule. Particular chemical procedures include for example those described in International Patent Specification Nos. WO 93/06231, WO 92/22583, WO 90/09195 and WO 89/01476 and the Examples herein utilising functional groups e.g. thiols in the protein and where necessary appropriately activated effector or reporter molecules, for example thiol selective derivatives such as maleimides where the target is a protein thiol group. Alternatively, where the effector or reporter molecule is a protein or polypeptide the linkage may be achieved using recombinant DNA procedures, for example as described herein or in International Patent Specification No. WO 86/01533 and European Patent Specification No. 392745.

The protein according to the invention may be useful in the detection or treatment of a number of diseases or disorders. Such diseases or disorders may include those described under the general headings of infectious disease, e.g. viral infection; inflammatory disease/autoimmunity e.g. rheumatoid arthritis, osteoarthritis, inflammatory bowel disease; cancer; allergic/atopic disease e.g. asthma, eczema; congenital disease, e.g. cystic fibrosis, sickle cell anaemia; dermatologic disease, e.g. psoriasis; neurologic disease, e.g. multiple sclerosis; transplants e.g. organ transplant rejection, graft-versus-host disease; and metabolic/ idiopathic disease e.g. diabetes.

The proteins according to the invention may be formulated for use in therapy and/or diagnosis and according to a further aspect of the invention we provide a pharmaceutical composition comprising a protein according to the invention together with a pharmaceutically acceptable excipient, diluent or carrier. As explained above, the protein in this aspect of the invention may be optionally linked to one or more effector or reporter groups.

The pharmaceutical composition may take any suitable form for administration, and, preferably is in a form suitable for parenteral administration e.g. by injection or infusion, for example by bolus injection or continuous infusion. Where the composition is for injection of infusion, it may take the form of a suspension, solution or emulsion in an oily or aqueous vehicle and it may contain formulatory agents such as suspending, preservative, stabilising and/or dispersing agents.

Alternatively, the protein composition may be in dry form, for reconstitution before use with an appropriate sterile liquid.

If the protein composition is suitable for oral administration the formulation may contain, in addition to the active ingredient, additives such as starch, e.g. potato, maize or wheat starch, or cellulose or starch derivatives such as microcrystalline cellulose; silica; various sugars such as lactose; magnesium carbonate and/or calcium phosphate. It is desirable that, if the formulation is for oral administration it will be well tolerated by the patient's digestive system. To this end, it may be desirable to include in the formulation mucus formers and resins. It may also be desirable to improve tolerance by formulating the protein in a capsule which is insoluble in the gastric juices. It may also be preferable to include the protein or composition in a controlled release formulation.

If the protein composition is suitable for rectal administration the formulation may contain a binding and/or lubricating agent; for example polymeric glycols, gelatins, cocoa-butter or other vegetable waxes or fats.

Therapeutic and diagnostic uses of proteins according to the invention typically comprise administering an effective amount of the protein to a human subject. The exact amount to be administered will vary according to the use of the protein and on the age, sex and condition of the patient but may typically be varied from about 0.1mg to 1000mg for example from about 1mg to 500mg. The protein may be administered as a single dose or in a continuous manner over a period of time. Doses may be repeated as appropriate. Typical doses may be for example between 0.1-50mg/kg body weight per single therapeutic dose, particularly between 0.1-20 mg/kg body weight for a single therapeutic dose.

The following Examples illustrate the invention. The following abbreviations are used:

AUC area under curve; β-ME β-mercaptoethylamine;
DCM Di-Fab' Maleimide; DTDP 4,4'dithiodipyridine;
Fab' antigen binding antibody fragment (with hinge);
$F(ab')_2$ dimeric Fab'; HC heavy chain; LC light chain;
NEM *N*-ethylmaleimide; PEG polyethylene glycol.

EXAMPLE 1

Evaluation of di-Fab' Production in *E.coli* utilising different hinge sequences.

Strategy - To minimise any possible incorrect interchain disulphide bonds between hinge regions and any other cysteines the interchain disulphide bond was removed from all Fab' constructs. It has been shown previously that removal of the interchain disulphide bond of a di-Fab' did not affect the stability of the protein as judged by serum permanence times (ref. 9). PCR mutagenesis was used to change the interchain cysteines of cKappa and C_H1 to serines. This also enabled analysis of % di-Fab' formation by analysing periplasmic extracts on non-reducing SDS-PAGE, followed by heavy chain (HC) specific western blotting. This approach thereby allowed analysis of many constructs at the shake flask scale. Advantage was taken of the mutagenesis of C_H1 to introduce a SpeI restriction site to facilitate rapid cloning of novel hinge sequences as annealed oligonucleotide cassettes. To introduce this site the Ser N-terminal to the interchain disulphide Cys in the heavy chain was changed to a Thr, hence changing the C-terminus of the C_H1 from ^{N}KSCDKTHTCAA^{C} to ^{N}KTSDKTHTCAA^{C} (changes underlined).

Bacterial strain and plasmid constructions - All final expression plasmids were based on pACYC184 [Yarranton, G.T. and Mountain A. (1992) in: Protein Engineering - a Practical Approach (Rees, AR., Stamberg, M.J.E. and Wetzel, R. eds) IRL Press, Oxford pp. 303-326) and used to transform W3110, wild type *E.coli* ATCC 27325.

A variant of A5B7g3 Fab' (graft number 3 of a humanised Fab' binding to CEA - carcinoembryonic antigen) lacking the interchain disulphide bond was first constructed. The interchain Cys codon in the light chain (LC) cKappa was changed by PCR mutagenesis to Ser using the mutagenic oligo:
5'-GCCGCGAATTCCGCACTTCTCCCTCTAAGACTCTCCCCTGTTGAAGCTC-3'.
A similar strategy was used to remove the interchain Cys codon from the C_H1 of the heavy chain (HC) and introduce the SpeI restriction site using the mutagenic oligo:
5'-CCGCAAGCTTGGATCCTCATCACGCGGCGCATGTGTGAGTTTTGTCACTAGTTT
TGGGCTCAACTTTC-3'
These and all subsequent clones were checked by DNA sequencing on an ABI 373A sequencer using PRISM cycle sequencing kit. Novel hinge sequences were produced by ligation of annealed oligonucleotide pairs with 5' SpeI-HindIII 3' ends via a similarly restricted A5B7g3 HC only plasmid, followed by reconstitution of the final dicistronic expression plasmid.

The coding region for Fab' 40.4 (a humanised Fab' binding a human cytokine) cKappa was similarly altered using the mutagenic oligonucleotide
5'-GGCCTGAGCTCACCAGTAACAAAAAGCTTTAATAGAGGAGAGTCTTGAGGAGGA
AAAAAAAATGAAG-3'.
A restriction fragment for the original Fab' hinge (^{N}CAA^{C}) C_H1 lacking the interchain disulphide bond cysteine was moved from A5B7g3 into the expression plasmid for Fab 40.4 as a restriction fragment. Since the SpeI site in the Fab 40.4 final expression plasmid pDPH40 was unique it was possible to make further hinge variants rapidly by directly ligating annealed oligonucleotide pairs with 5' SpeI-NotI 3' overhangs into similarly restricted pDPH40. Details of the hinge sequences and plasmids are shown in Table I. During DNA manipulation steps preferred codons for E.coli as defined by Wada, K.N. *et al. Nucleic Acids Res.* (1991) 19, 1981 were chosen.

Shake flask experiments - Shake flask experiments were conducted essentially as described previously except that these were single plasmid experiments and required Tetracycline at 10μgml^{-1} [Humphreys, D.P. *et al.*, FEBS Lett. (1996), 380, 194]. L-

Broth was used for all experiments with A5B7, and in order to give the highest possible cell density, 2xTY was used for those with Fab 40.4. Redox active compounds were added as solids to a final concentration of 1mM when required. Samples were taken at 0, 1, 2, and 4 hours post-induction.

Fermentation - synthetic SM6 C media: (5.0 g/L $(NH_4)_2SO_4$, 3.312g/L $Na_2H_2PO_4.H_2O$, 3.870g/L KCl, 1.0g/L $MgSO_4.7H_2O$, 1.0 g/L Citrate, 4.00g/l Citric acid, 0.05 g/L $CaCl_2.6H_2O$, 0.02 g/L $ZnSO_4.4H_2O$, 0.02 g/L $MnSO_4.4H_2O$, 0.005 g/L $CuSO_4.5H_2O$, 0.004 g/L $CoSO_4.6H_2O$, 0.0967 g/L $FeCl_3.6H_2O$, 0.0003 g/L H_3BO_3, 0.0002 g/L $NaMoO_4$). Glycerol was used as a carbon source at 3% (w/v) and MAZU was used as an antifoam at 0.02% (v/v). pH was controlled with 50% (v/v) NH_4OH. Fab' expression was induced by switching of the carbon source to lactose at 5% (w/w), cells were harvested 24-36 hours post-induction. Fab' yields were typically 100-150mg/L.

Western blotting - Samples equivalent to 2l of periplasmic fractions were diluted 5 fold with dH_2O and boiled for 5 minutes in non-reducing SDS-PAGE loading buffer, before being electrophoresed on 4-20% Tris-glycine gels (Novex) at 125v for 1.75 hours. The proteins were transferred to a PVDF membrane (Novex) for 2 hours at 100mA. The membrane was blocked for 1 hour at room temperature with 50ml per membrane of 'blocking buffer' (PBS / 0.1% (v/v) Tween 20 / 2% (w/v) skimmed milk), before shaking at room temperature for 1 hour with 5ml per membrane of anti Fd antibody (Sheep IgG anti Human IgG(Fd), ref. PC075, The Binding Site, Birmingham, U.K.) at 1/1000 (v/v) in 'antibody buffer' (PBS / 0.1% (v/v) Tween 20 / 0.1% 'blocking buffer'). The membrane was washed extensively in PBS / 0.1% (v/v) Tween 20, before shaking at room temperature for 1 hour with 5ml per membrane of a donkey anti sheep HRP conjugated antibody (Rabbit $F(ab')_2$ anti Sheep IgG Fc fragment HRP conjugate, ref. 313-036-046, Jackson) at 1/1000 (v/v) in 'antibody buffer'. The membrane was washed extensively in PBS / 0.1% (v/v) Tween 20, before development with DAB substrate (Pierce). LC cross reactive bands are shown by lanes 4 and 1 of Figures 1 and 2 respectively. Life size positive transparencies of blots were used for laser scanning densitometry on a Molecular Dynamics model 300A machine using ImageQuant software version 4.2. Di-Fab derived heavy chains (di-HC) separate from Fab derived HC (free HC) during electrophoresis. Quantitation of the relative intensities of the two easily identifiable bands in each lane gave an estimate of the % di-Fab formed. This assumes a relatively constant level of production of HC and its association with LC between different Fab' variants. The pTTO-1 derived plasmids used produce an excess of LC, and so free HC in the

periplasm is undetectable (Shauna West, personal communication). Di-HC of proteins lacking the interchain disulphide migrate with a mobility similar to a purified Fab' standard with the interchain disulphide (compare lane 11 and 3 of Figure 1). The total absorbance of each peak was quantified, and the % of di-Fab in each sample was calculated thus: absorbance of di-HC band ÷ absorbance of di-HC band + absorbance of HC band.

Fab' purification - Periplasmic extracts were clarified by centrifugation at 25,000g for 30 minutes, the pH was increased to 6.5 with 2.5M Tris, and applied to a ProteinG sepharose (GammaBind, Pharmacia Biotech) column pre-equilibrated with P.B.S. After washing with P.B.S. to remove unbound material, the Fab' related material was eluted by washing the column with 0.1M Glycine.Cl pH 2.7. The pH of the eluate was increased to neutral with 2.5M Tris for storage at 4°C, Fab' concentrations after purification were typically $\leq$0.2 $mgml^{-1}$.

Plasmids were constructed with two copies of the repeat sequence TCPPCPA with between 0 and 5 spacing residues, see pDPH30-35, Table I (Fab' construct nomenclature shows the number of middle hinge sequence repeats, followed by Roman numerals to show the number of spacing residues, and whether the protein has or lacks the interchain disulphide bond forming cysteine. For example, pDPH34 expresses A5B7g3 hinge 2iv inter = graft 3 of A5B7 with two hinge repeats, spaced by four aminoacids and lacking the interchain disulphide bond. pDPH42 expresses Fab' 40.4 hinge 2o + Cys, has two hinge repeats, with no spacing residues and having the interchain disulphide bond). These were evaluated for their ability to form di-Fab's in shake flask cultures as judged by western blotting and compared against the hinge $^1/_2$ and hinge 1 constructs. The results are shown in Table II.

Similar to that seen by others (ref. 7), the hinge $^1/_2$ Fab' produced no detectable di-Fab' in shake flasks. 'hinge 1' and 'hinge 2o' produced a moderate amount of di-Fab' (7.3% and 4.8% respectively). These versions were then made in the more highly expressed Fab 40.4, to see if increasing the periplasmic protein concentration of these Fabs would effect both an increase in di-Fab' formation *in vivo*, and discriminate the relative merits of an increasing number of hinge repeats.

It was surprising to see that all of the A5B7 constructs with spacing residues between the hinge repeats produced no detectable di-Fab'. The increasing length and flexibilty of these spacing regions could allow the second copy of the hinge repeat to fold back and form intra-HC disulphide bonds, thereby masking the cysteines from forming the

desired inter-HC disulphide bonds. Although it is difficult to prove this assumption directly, two new constructs were designed using Fab 40.4 with reduced spacing/flexibility by removing one (Ala) or two (Ala-Thr) of the endogenous spacing residues between the rigid polyproline II helixes. The results for these as shown in Table II were not favourable, so a Fab' 40.4 with three copies of the hinge, 'hinge 3o' was made

The results show that an increase in the number of copies of hinge repeats result in a steady decrease in the % of di-Fab' produced. This decrease in % di-Fab' can be presumed to be due to increasing toxicity of the protein in the periplasm as the proteins become more cysteine rich. The decrease in % di-Fab' correlated with decreased cell viability post-Fab' induction as shown by lower peak $O.D._{600}$'s and increased cell lysis at the later time points. The disulphide redox machinery in the *E.coli* periplasm is now well understood, but it is thought to be less well adapted to cope with proteins having complex disulphide arrangements than that of the endoplasmic reticulum (reviewed by Humphreys *et al.*, 1996 *ibid*). It seems likely that complex hinges are not well tolerated.

Reduction of the spacing between two hinge repeats does not increase di-Fab' formation. 'Fab' 40.4 inter hinge 2_{-1}' shows decreased di-Fab' compared to the 'hinge 2o' variant (8.1 % ± 4.3 compared to 25.1 % 8.43 - see Table II). 'Fab' 40.4 inter hinge 2_{-2}' shows 49.8 % ±16.78 di-Fab'. This figure suggests a high level of di-Fab' production. In fact this protein appears unable even to produce substantial amounts of full length Fab', this is demonstrated by the increased number and intensity of proteolytic bands in lane no. 7 of the western blot shown in Figure 1. Hence there is a small amount of di-Fab' which is high relative to the amount of Fab', but very little of either protein is produced relative to 'hinge 1' and 'hinge 2o'. It can be postulated that removing one or both of these spacing residues makes the hinge regions so inflexible that the cysteines are forced into a conformation that makes them proteolytically exposed or reactive to native *E.coli* proteins. Since the unmodified 1 hinge gave the greatest di-Fab' yield *in vivo*, it was decided to test other hinge isotypes for their effectiveness.

Effect of hinge isotype - True hinge sequences for the IgG2, 3, and 4 could not be created, but rather the middle hinge of each was fused onto the existing IgG1 upper hinge. The hinges created are therefore called IgG2 'like'. Since long cysteine rich hinges are poorly tolerated, only the CPRC and the first of the three repeating sequences of the IgG3 middle hinge were used. The prime superscript is used to

show that this IgG3 sequence was truncated. These constructs were analysed in the same way previously, and the results are shown in Table II.

The IgG3' like hinge was poorly tolerated and so gave an artifactually high % di-Fab' measurement in the same way that hinge 2_{-2} did, an example of this proteolysis is shown in lane 4 of Figure 2. The long IgG3 hinge is thought to be highly flexible [Brekke, O.H. *et al* (1995) Immunol. Today 16, 85] and this is responsible for some of the properties of this isotype. In the periplasm this length of exposed peptide is likely to be susceptible to proteolysis, and this may be the reason for the poor level of production of this protein. The IgG 2 like hinge produced a reasonable amount of di-Fab' (20.8 % ± 3.58), but gave no increase over that seen before with the IgG 1 derivatives. A relative inability of the IgG 4 like Fab' to produce di-Fab' (8.63 % ± 1.41) was oberved. There is only one amino acid difference between the IgG 4 like hinge and the IgG1 hinge - CPSP relative to CPPC respectively. The results are consistent with previous work (ref. 22, 23), which found that IgG 4 was less able to form inter-HC disulphide bonds than IgG1. The presence of a serine between the two cysteines may allow increased flexibility of the middle hinge, and thereby formation of intra-HC disulphides which block inter-HC disulphide formation.

Effect of IgM and IgA tailpieces - IgM and IgA both have 18 amino-acid C-terminal extensions called secretory tailpieces that are involved in their polymerisation. The penultimate residue for both tailpieces is a cysteine. This and other HC cysteines, along with non-covalent interactions are known to be involved in polymer formation, although the exact disulphide organisation is not completely understood [Davis, A.C. *et al.*, (1989), EMBO J. 8, 2519 and Wiersma, E.J. and Shulman, M.J. (1995) J. Immunol. 154, 5265]. The tailpiece has been added to all four IgG isotypes and effected their polymerisation even in the absence of the additional HC cysteines and non-covalently interacting residues found in IgM and IgA [Smith, R.I.F. *et al* (1995) J. Immunol. 154, 2226]. The wild type and tailpiece sequences described by Sørensen, V. *et al.*, (1996) J. Immunol. 156, 2858] were added to Fab' 40.4 containing a 'hinge 1' sequence. The 'hinge 1' sequence was chosen since it seemed possible that at least one free cysteine might be required to act as a mimic of Cys^{414} of IgM to provide for tailpiece-HC, and one other to allow for direct inter-HC interactions such as thought to be provided for by Cys^{337} of IgM. The sequences constructed in pDPH 50 and 51 are shown in Table I.

The Fab's were analysed by shake flask culture/western blotting for the presence of increased polymer formation. Although 'hinge 1' was known to give ~30% di-Fab'

formation, it was found that the presence of either of the tailpieces completely abolished di-Fab' formation. No evidence was found for the formation of higher polymeric states as judged by western blots of non reducing native and SDS PAGE. It was assumed that the abolition of dimer formation inherent to 'hinge 1' was due to folding back of the tailpieces to form an intra-HC disulphide between the tailpiece Cys and one of those in the hinge. This seems quite possible as the tailpiece sequences are thought able to form one beta strand, allowing the tailpiece Cys to be close to the hinge [Pumphrey, R. (1986) Immunol. Today 7, 174].

In general, the results show that the presence of extra hinge cysteines above the single one found in the original Fab' was the most important factor in promoting di-Fab' formation *in vivo*, with 'Hinge 1' and 'hinge 2o' being the best sequences. No benefit was found with other versions of the 1 hinge over these, nor with any of the other 3 IgG isotypes tested. Simple hinges proved to be the most useful, with increasing length of hinge producing less % di-Fab' and a higher cell mortality. This was seen both with increasing copy number of the IgG1 hinge sequence i.e. hinge 1, 2o, and 3o, and with the long and flexible truncated IgG3.

More subtle structural differences also affected the efficiency of di-Fab' formation *in vivo*. Manipulation of the spacing residues between two copies of the hinge sequence ^{N} TCPPCPA ^{C} implied the importance of conformation for maintaining the hinge cysteines in a di-Fab' forming state. If the spacing region became too long, di-Fab' formation was completely abolished, presumably by looping back of the hinge masking hinge cysteines, whilst if the spacing was too short, the hinge was badly degraded *in vivo*.

Previous reports found variable production of di-Fab' from high cell density fermentaion of 5-70% using the hinge sequence ^{N}CPPCPPCPP^{C} (ref. 9). The results herein demonstrate that it is very difficult to produce greater than 5-10 % di-Fab' *in vivo* from fermentations and that this is reproducible. In addition to the hinge sequence, these differences may be accounted for by differences in Fab' expression levels, fermentation conditions and host strain. The Fab' yield here was 5 to 10 fold lower than that described by Rodrigues *et al.*, (ref. 9). However, it is known that specific conditions can cause a spontaneous, high efficiency (~80%), and batch specific di-Fab' formation during purification. Such protein purification conditions were not used during these small scale experiments.

In summary, di-Fab' formation *in vivo* in the periplasm of *E.coli* is an inefficient process that is modulated *inter alia* by hinge sequence and complexity. Two hinge sequences ('hinge 1' and 'hinge 2o') have been identified under *in vivo* selection conditions to be the most efficient for di-Fab' formation.

EXAMPLE 2

Investigation of serum permanence times and hinge specific pegylation of $F(ab')_2$ molecules with modified hinges

Reagents

NEM, β-MA, DTDP, and Tris were from Sigma (UK) and of the highest grade available. Pyrogen free 'Flowfusor' water was used for chromatography (Fresenius, Basingstoke, UK). All other laboratory reagents were reagent grade from BDH (UK).

Production and Purification of Fab'

The Fab' used was 'Fab 40.4', as described in Example 1. Fab' fermentations and Protein G sepharose purifications (GammaBind Plus, Pharmacia Biotech) were as described in Example 1, with one modification. *E.coli* periplasmic proteins were extracted from fermentation cell paste by overnight incubation at 30°C and with shaking at 250 rpm in one fermentation harvest volume of 100mM Tris/10mM EDTA (pH 7.4). The conductivity and pH of the crude extract were altered to $\leq$ 3.5mS cm^{-1} and $\leq$ 4.5 by addition of water and glacial acetic acid respectively. Crude extract was then passed over an 80ml (compacted) bed volume of Streamline SP cation exchange resin (Pharmacia Biotech) in expanded bed mode. The resin was pre-equilibrated with 50mM sodium acetate pH 4.5 in expanded bed mode. After extensive washing, bound material was eluted in compacted mode with 50mM sodium acetate/200mM NaCl pH 4.5. The pH of the peak fraction was increased to $\geq$ 6.5 with 2.5M Tris, and applied to a Protein G sepharose column pre-equilibrated with PBS. After washing with PBS to remove unbound material, the Fab' material was eluted with 0.1M Glycine Cl pH 2.7. The eluate was neutralised with 2.5M Tris for storage at 4°C.

Production and Purification of $F(ab')_2$

Fab' material was concentrated and buffer exchanged to $\geq$ 12 $mgml^{-1}$ in 0.1M sodium phosphate buffer pH 8.0 using ultra-filtration with a 10kDa cut-off membrane. Hinge thiols were activated and traces of $F(ab')_2$ depending upon final protein concentration) were removed by reduction with 9-mM β-MA in 0.1M sodium phosphate buffer pH 8.0 for 45 min. at 37°C. Reductant was removed by desalting on a G25M sephadex column (PD10), (Pharmacia Biotech) pre-equilibrated with

0.1M sodium phosphate buffer pH 8.0. $F(ab')_2$ was allowed to form by incubation at room temperature overnight. Any remaining thiol groups were blocked by incubation with 10mM NEM in PBS before analysis by SDS-PAGE (4-20% Tris/glycine gels, Novex UK) and HPLC (GF-250 column equilibrated with 0.2M sodium phosphate buffer pH 7.0).

$F(ab')_2$ was separated from Fab' on a small scale by collecting preparative HPLC fractions (GF-250XL column equilibrated with 0,2M sodium phosphate buffer pH 7.0), or on a large scale using hydrophobic interaction chromatography (HIC). Solid $(NH_4)_2SO_4$ was added to Fab'/$F(ab')_2$ mixtures to 0.75M before loading onto a phenyl-sepharose HP column (Pharmacia Biotech) equilibrated with 50mM phosphate buffer pH 7.0/0.75M $(NH_4)_2SO_4$. After washing with equilibration buffer, bound material was eluted with 50mM sodium phosphate buffer pH 7.0. The dimeric species has a higher affinity for the HIC matrix than the monomeric Fab'. All purified $F(ab')_2$ was judged to be 100% $F(ab')_2$ by HPLC and $\geq$ 95% $F(ab')_2$ by Coomassie stained SDS-PAGE.

Production of chemically cross linked $F(ab')_2$ (DFM)

DFM was produced as described previously using 1,6-bismaleimido-hexane (BMH) cross-linker (ref. 2).

Resistance to reduction of $F(ab')_2$

Purified $F(ab')_2$ at 0.25 $mgml^{-1}$ in 0.1M phosphate pH 7.0 was treated with β-MA from 0 to 2mM for 45min at 37°C. Reductions were stopped by addition of NEM to 10mM and the relative amounts of $F(ab')_2$ and Fab' calculated by HPLC analysis.

Partial reduction of 'Hinge 2o' $F(ab')_2$ for hinge specific modification

Purified $F(ab')_2$ at 6$mgml^{-1}$ in 0.1M phosphate pH 6.0 was treated with β-MA from 0 to 2mM for 45 min. at 37°C. The reductant was removed by desalting with a P6 Biospin column (BioRad, UK) and samples taken immediately for thiol assay, NEM quenching and HPLC analysis and modification. 1.3mM β-MA was used for all preparative partial reductions.

Production and Catin Exchange Purification of $F(ab')_2$

PEG-$F(ab')_2$ partially reduced as above was mixed with an equal volume of 25kDa linear PEG-maleimide in 0.1M phosphate pH6.0 (Shearwater Polymers Inc, Birmingham, Alabama, USA) to give a final molar excess of PEG:$F(ab')_2$ of 30 fold. After reacting overnight at room temperature, $F(ab')_2$-PEG was separated from the

bulk of remaining $F(ab')_2$ using preparative scale HPLC. After concentration, and buffer exchange using a PD 10 column to 50mM sodium acetate pH 4.5, the $F(ab')_2$-PEG/ unreacted PEG fraction was loaded on to a 1.6ml bed volume Poros HS column (PerSeptive Biosystems, Hertford, UK) on a BioCad Vision workstation. After washing with 5 column volumes to remove unbound PEG-maleimide, $F(ab')_2$-PEG was eluted with 50mM sodium acetate/ 40mM NaCl pH4.5, and $F(ab')_2$ was removed from the column with a linear gradient of 50mM sodium acetate pH 4.5 with NaCl from 40mM to 1M. Fractions were concentrated and buffer exchanged to 0.2M sodium-phosphate buffer pH 7.0 before estimating protein concentrations using A_{280}. Protein was analysed by SDS-PAGE ujsing 4-12% Tris-MES gels (Novex, UK).

Thiol assay

Thiols per $F(ab')_2$ were determined using DTDP as described previously (ref. 17).

Iodination of $F(ab')_2$

300μg of $F(ab')_2$ per animal group was ^{125}I-labelled using Bolton and Hunter reagent (Amersham) to a specific activity of 0.22-0.33 μCi/μg.

Mass Spectrometry

Molecular masses for Fab' was determined used Fisons VG Quattro triple quadrupole equipment in electrospray ionisation mode.

Animal studies

Male Sprague Dawley rats of 220-250g (Harlan) were injected *intra venously* with 20μg ^{125}I-labelled Fab 40,4 $F(ab')_2$ hinge variants whilst under Halothane anaesthesia (n=6 per group, except for 'hinge 20' where n = 10). Serial arterial bleeds from the tail were taken at 0.5, 2, 4, 6, 24, 48, 72 and 144 hours post administration. Samples were counted using a COBRA™ Autogamma counter (Canberra Packard). Data were plotted and Area Under Curve were calculated using GraphPad Prism (GraphPad Software Incorporated) and is expressed as % injected dose hour (% id.hr). The $t^1/_2\beta$ is defined by time points 24, 48, 72. The means and standard errors of means (SEM) of data are shown.

RESULTS

Production of $F(ab')_2$ *in vitro*

Three hinge sequences were used to produce $F(ab')_2$ *in vitro* : 'hinge $^1/_2$'= ^{N}THTCAA^C; 'hinge 1' = ^{N}THTCPPCPA^C; and 'hinge 2o'= ^{N}THTCPPCPATCPPCPA^C. These contain 1, 2 and 4 hinge cysteines respectively.

The 'hinge 1' and 'hinge 2o' proteins also contain one amino acid difference over 'hinge $^1/_2$' of a Ser to Thr change in the C-terminus of C_H1 as described in Example 1.

After purification and concentration at pH 8.0 the Fab's were found to contain significant amounts of $F(ab')_2$. In order for the $F(ab')_2$ product to be as homogeneous as possible the Fab' preparations were subjected to identical strongly reducing conditions (80mM β–MA, pH 8.0) so that the oxidation process started from 100 % Fab'. Antigen binding analysis (BIAcore) of $F(ab')_2$ show that these very strong reducing conditions do not affect Fab affinity for soluble antigen. Reduced and desalted Fab' was left at room temperature overnight for maximum $F(ab')_2$ yield. However, by taking samples during the oxidation for quenching with NEM it could be seen that aprproximately 60% of achievable $F(ab')_2$ forms within the first 60 minutes of the oxidation - see Figure 3. Both 'hinge $^1/_2$' and 'hinge 2o' reached similar final yields of ~65% with an overnight incubation, however, $F(ab')_2$ formation within the first 30 minutes was more rapid for 'hinge 2o' than 'hinge $^1/_2$'. This is probably a consequence of the greater number of hinge cysteines increasing the chances of Fab'-Fab' hinge cysteine interactions occurring. The yield of $F(ab')_2$ using 'hinge 2o' can be increased to 80% simply by increasing the concentration of Fab' to $\geq$20mgml^{-1}.

It was surprising that 'hinge 1' did not reach the same final yields of $F(ab')_2$ formation as the other two proteins. It is possible that after reduction a percentage of 'hinge 1' rapidly undergoes intra-hinge disulphide formation, thereby capping the thiols off from inter-hinge disulphide formation.

No C-terminal proteolysis was observed with purified 'hinge 1' or hinge 2o' $F(ab')_2$, removing the possibility that a proportion of 'hinge' molecules have a cysteine missing. HC from reduction of both 'hinge1' and 'hinge 2o' were shown by mass spectrometry to be full length molecules - 'hinge 1' had an observed mass of 24703.65 ± 0.55 Da relative to the predicted mass of 24705.12 Da, 'hinge 2o' had an observed mass of 25366.40 ± 6.13 Da relative to the predicted mass of 25374.88 Da.

Number of disulphide bonds in $F(ab')_2$ hinge regions

'Hinge $^1/_2$' $F(ab')_2$ has an advantage over 'hinge 1' and 'hinge 2o' in that the product of hinge disulphide bond formation is homogeneous. In contrast 'hinge 1' may be able to form three different species of $F(ab')_2$ with a mixture of single and double disulphide and 'head to head' and 'head to tail' species (see Figure 4). The picture is potentially even more complex with 'hinge 2o'. Consideration of the primary sequence (in the absence of modelling predictions) shows a large number of species that could be

formed. These differ in the number of disulphide bonds (between one and four), staggered linear arrangements, and gross quaternary structure (both 'head to head' and 'head to tail' formations). Rotation around a disulphide bond makes it seem unlikely that single disulphide bonded forms of 'hinge 2o' could survive more than transiently in the absence of thiol capping agents.

With $F(ab')_2$ produced *in vivo* in *E.coli*, the presence of more hinge cysteines does not result *per se* in a highly disulphide bonded hinge (ref. 9). Hence it was important to demonstrate whether the two larger hinges contained more than one disulphide bond. Advantage was taken of an observation made whilst optimising reduction/oxidation conditions that 'hinge 2o' required a higher β-MA concentration in order to reduce all of the contamainating $F(ab')_2$ in the purified Fab'. It was possible that the different purified $F(ab')_2$ proteins would exhibit differences in their ability to resist reduction to Fab'. It was found that at 0.25 $mgml^{-1}$ and pH 7.0 'hinge $^1/_2$' is completely reduced by 125μM β-MA (see Figure 5). At the same concentration of β-MA 68.3% of the 'hinge 1' preparation is still dimeric. This implies that approximately 68% of the population of 'hinge 1' $F(ab')_2$ has two disulphide bonds. At the slightly greater β-MA conncentration of 166μM, 100% of the 'hinge 2o' preparation is still dimeric. Hence by extrapolation, >68% of 'hinge 2o' molecules must have more than 2 disulphide bonds i.e. 3 or 4. Although hinge structural differences might have an effect on the accessibility or chemical reactivity of hinge disulphides, it seems unlikely that they would be significant enough to cause the gross differences seen in Figure 5. Hence 'hinge 1' and 'hinge 2o' have a high degree of multiple disulphide bonding.

Effect of hinge sequence of $F(ab')_2$ pharmacokinetics in Rat

$F(ab')_2$ made from all three hinge constructs along with a DFM control were ^{125}I-labelled so that their pharmacokinetics could be followed in a rat model. The data shown in Table III support the comparisons made *in vitro* between hinges $^1/_2$, 1, and 2o. $F(ab')_2$ with a single hinge disulphide 'hinge $^1/_2$' is cleared most rapidly from the circulation, with an AUC of 166.2 ± 9.8% injected dose. hour (% id.hr). $F(ab')_2$ with an identical protein sequence, but linked by thioether bonds is cleard more slowly, AUC = 384.2 ± 32.1 (% id.hr). This is interpreted as evidence of the greater lability of the disulphide over thioether linkage, leading to a more rapid breakdown *in vivo* to Fab'. The smaller Fab' is excreted more rapidly through the kidneys than $F(ab')_2$. Increase of the average number of disulphide bonds in the hinge with 'hinge 1' and 'hinge 2o' results in increased AUC (423.6 ± 35.0 and 509.7 ± 31.3 (%id.hr) respectively) over that of 'hinge $^1/_2$'. The curves for clearance from circulation of rats for the four $F(ab')_2$ molecules tested are shown in Figure 6. This demonstrates graphically that the major

effect of the different hinge stabilities appears to be on the α-phase. The initial clearance of 'hinge $^1/_2$' $F(ab')_2$ is much more rapid than the other three $F(ab')_2$ molecules which are more grouped together. Presumably increased resistance of 'hinge 1', 'hinge 2o' and DFM $F(ab')_2$ to reductive or proteolytic forces in circulating blood leads to the molecules surviving for longer as the larger $F(ab')_2$ species which is cleared more slowly from the circulation.

Partial Reduction and PEGylation of 'Hinge 2o' $F(ab')_2$ *in vitro*

Since the 'hinge 2o' $F(ab')_2$ has a large proportion of molecules with multiple hinge disulphides, it seemed possible that a number of disulphide bonds could be broken and uncoupled thiols activated whilst retaining the molecule as a dimeric species. Such thiols would be particularly useful for attachment of effector or reporter groups such as radionucleotides, toxins, or PEG. Covalent attachment of PEG to proteins is attractive since it is a simple route to increasing the serum permanence, reducing immunogenicity, and decreasing proteolysis *in vivo*.

Using a range of β-ME concentrations at pH 6.0 and analysis of NEM quenched samples of HMPC it was found that at ≤1.8mM β-ME 100% of the $F(ab')_2$ population remained dimeric. This figure may vary between batches of $F(ab')_2$ due to hinge disulphide occupancy heterogeneity. At 1.3mM β-ME thiol assay with DTDP showed 1.034 ± 0.090 thiols per $F(ab')_2$ being liberated for reaction . $F(ab')_2$ not treated with β–ME showed little free thiols per $F(ab')_2$. The efficiency of PEGylation of $F(ab')_2$ was calculated after purification of $F(ab')_2$-PEG by cation exchange and estimation of protein concentration by A_{280} to be ≤ 1.3%.

Table I. Oligonucleotide cassettes for construction of hinge sequences.

Plasmid name and oligonucleotide cassette and hinge sequence

pDPH28 A5B7g3 hinge ½ Δinter

```
5' ACT AGT GAC AAA ACT CAC ACA TGC GCC GCG TGA TGA GGA TCC AAG CTT      3'
     T   S   D   K   T   H   T   C   A   A   *   *
```

pDPH29 A5B7g3 hinge 1 Δinter

```
5'  CT AGT GAC AAA ACT CAC ACC TGC CCG CCG TGC CCG GCG TGA TGA GGA TCC A      3'
3'       A CTG TTT TGA GTG TGG ACG GGC GGC ACG GGC CGC ACT ACT CCT AGG TTC GA 5'
     T   S   D   K   T   H   T   C   P   P   C   P   A   *   *
```

pDPH30 A5B7g3 hinge 2o Δinter

```
5'  CT AGT GAC AAA ACT CAC ACC TGC CCG CCG TGC CCG GCG ACC TGC CCG CCG TGC CCG GCG TGA TGA GGA TCC A      3'
3'       CA CTG TTT TGA GTG TGG ACG GGC GGC ACG GGC CGC TGG ACG GGC GGC ACG GGC CGC ACT ACT CCT AGG TTC GA 5'
     T   S   D   K   T   H   T   C   P   P   C   P   A   T   C   P   P   C   P   A   *   *
```

pDPH31 A5B7g3 hinge 2i Δinter

```
5'  CT AGT GAC AAA ACT CAC ACC TGC CCG CCG TGC CCG GCG GGA ACC TGC CCG CCG TGC CCG GCG TGA TGA GGA TCC A      3'
3'       CA CTG TTT TGA GTG TGG ACG GGC GGC ACG GGC CGC CCT TGG ACG GGC GGC ACG GGC CGC ACT ACT CCT AGG TTC GA 5'
     T   S   D   K   T   H   T   C   P   P   C   P   A   G   T   C   P   P   C   P   A   *   *
```

pDPH32 A5B7g3 hinge 2ii Δinter

```
5' CT AGT GAC AAA ACT CAC ACC TGC CCG CCG TGC CCG GCG GGA GGA ACC TGC CCG CCG TGC CCG GCG TGA TGA GGA TCC A      3'
3'       CA CTG TTT TGA GTG TGG ACG GGC GGC ACG GGC CGC CCT GGA TGG ACG GGC GGC ACG GGC CGC ACT ACT CCT AGG TTC GA 5'
    T   S   D   K   T   H   T   C   P   P   C   P   A   G   G   T   C   P   P   C   P   A   *   *
```

Table 1 (continued)

pDPH33 A5B7g3 hinge 2iii Δinter

```
5'  CT AGT GAC AAA ACT CAC ACC TGC CCG CCG TGC CCG GCG GGA GGA GGA ACC TGC CCG CCG TGC CCG GCG TGA TGA GGA
3'      CA CTG TTT TGA GTG TGG ACG GGC GGC ACG GGC CGC CCT GGA GGA TGG ACG GGC GGC ACG GGC CGC ACT ACT CCT
    T   S   D   K   T   H   T   C   P   P   C   P   A   G   G   G   T   C   P   P   C   P   A   *   *

TCC A      3'
AGG TTC GA 5'
```

pDPH34 A5B7g3 hinge 2iv Δinter

```
5'  CT AGT GAC AAA ACT CAC ACC TGC CCG CCG TGC CCG GCG GGA GGA GGA GGA ACC TGC CCG TGC TGC CCG GCG TGA TGA GGA
3'      CA CTG TTT TGA GTG TGG ACG GGC GGC ACG GGC CGC CCT GGA GGA GGA TGG ACG GGC ACG ACG GGC CGC ACT ACT CCT
    T   S   D   K   T   H   T   C   P   P   C   P   A   G   G   G   G   T   C   P   C   C   P   A   *   *

TCC A      3'
AGG TTC GA 5'
```

pDPH35 A5B7g3 hinge 2v Δinter

```
5'  CT AGT GAC AAA ACT CAC ACC TGC CCG CCG TGC CCG GCG AAA GGC AAA GGC GAA ACC TGC CCG TGC TGC CCG GCG TGA TGA
3'      CA CTG TTT TGA GTG TGG ACG GGC GGC ACG GGC CGC TTT CCG TTT CCG CTT TGG ACG GGC ACG ACG GGC CGC ACT ACT
    T   S   D   K   T   H   T   C   P   P   C   P   A   K   G   K   G   E   T   C   P   C   C   P   A   *   *

GGA TCC A      3'
CCT AGG TTC GA 5'
```

pDPH40 Fab 40.4 hinge ½ Δinter

```
5'  CT AGT GAC AAA ACT CAC ACA TGC GCC GCG TGA TGA GGA TCC AAG CTT GC      3'
3'      A CTG TTT TGA GTG TGT ACG CGG CGC ACT ACT CCT AGG TTC GAA CGC CGG 5'
    T   S   D   K   T   H   T   C   A   A   *   *
```

pDPH41 Fab 40.4 hinge 2o Δinter

```
5'  CT AGT GAC AAA ACT CAC ACA TGC CCG CCG TGC CCG GCG ACC TGC CCG CCG TGC CCG GCG TGA TGA GGA TCC A      3'
3'      A CTG TTT TGA GTG TGT ACG GGC GGC ACG GGC CGC TGG ACG GGC GGC ACG GGC CGC ACT ACT CCT AGG TTC GA 5'
    T   S   D   K   T   H   T   C   P   P   C   P   A   T   C   P   P   C   P   A   *   *
```

Table 1 (continued)

pDPH42 Fab 40.4 hinge 2o +Cys

```
5' ACT TGT GAC AAA ACT CAC ACA TGC CCG CCG TGC CCG GCG ACC TGC CCG CCG TGC CCG GCG TGA TGA GGA TCC A 3'
     T   C   D   K   T   H   T   C   P   P   C   P   A   T   C   P   P   C   P   A   *   *
```

pDPH44 Fab 40.4 hinge 1 Δinter

```
5'  CT AGT GAC AAA ACT CAC ACA TGC CCG CCG TGC CCG GCG TGA TGA GGA TCC A      3'
3'       A CTG TTT TGA GTG TGT ACG GGC GGC ACG GGC CGC ACT ACT CCT AGG TTC GA 5'
     T   S   D   K   T   H   T   C   P   P   C   P   A   *   *
```

pDPH52 Fab 40.4 hinge 1 +Cys

```
5' ACT TGT GAC AAA ACT CAC ACA TGC CCG CCG TGC CCG GCG TGA TGA GGA TCC A      3'
     T   C   D   K   T   H   T   C   P   P   C   P   A   *   *
```

pDPH53 Fab 40.4 hinge 2_{-1} Δinter

```
5'  CT AGT GAC AAA ACT CAC ACA TGC CCG CCG TGC CCG ACC TGC CCG CCG TGC CCG GCG TGA TGA GGA TCC A      3'
3'       A CTG TTT TGA GTG TGT ACG GGC GGC ACG GGC TGG ACG GGC GGC ACG GGC CGC ACT ACT CCT AGG TTC GA 5'
     T   S   D   K   T   H   T   C   P   P   C   P   T   C   P   P   C   P   A   *   *
```

Table 1 (continued)

pDPH54 Fab 40.4 hinge 2_2 Δinter

```
5'  CT AGT GAC AAA ACT CAC ACA TGC CCG CCG TGC CCG TGC CCG CCG TGC CCG GCG TGA TGA GGA TCC A      3'
3'       A CTG TTT TGA GTG TGT ACG GGC GGC ACG GGC ACG GGC GGC ACG GGC CGC ACT ACT CCT AGG TTC GA 5'
     T   S   D   K   T   H   T   C   P   P   C   P   C   P   P   C   P   A   *   *
```

pDPH69 Fab 40.4 hinge 3o Δinter

```
5'  CT AGT GAC AAA ACT CAC ACC TGC CCG CCG TGC CCG GCG ACC TGC CCG CCG TGC CCG GCG ACC TGC CCG CCG TGC CCG GCG
3'       CA CTG TTT TGA GTG TGG ACG GGC GGC ACG GGC CGC TGG ACG GGC GGC ACG GGC CGC TGG ACG GGC GGC ACG GGC CGC
     T   S   D   K   T   H   T   C   P   P   C   P   A   T   C   P   P   C   P   A   T   C   P   P   C   P   A

TGA TGA GGA TCC AAG CTT GC      3'
ACT ACT CCT AGG TTC GAA CGC CGG 5'
  *   *
```

pDPH50 Fab 40.4 hinge 1 Δinter IgMtp

```
5'  CT AGT GAC AAA ACT CAC ACC TGC CCG CCG TGC CCG GCG GGC AAA CCG ACC CTG TAT AAC GTG AGC CTG GTG ATG AGC GAT
3'       CA CTG TTT TGA GTG TGG ACG GGC GGC ACG GGC CGC CCG TTT GGC TGG GAC ATA TTG CAC TCG GAC CAC TAC TCG CTA
     T   S   D   K   T   H   T   C   P   P   C   P   A   G   K   P   T   L   Y   N   V   S   L   V   M   S   D

ACC GCG GGC ACC TGT TAT TGA TGA GGA TCC AAG CTT GC      3'
TGG CGC CCG TGG ACA ATA ACT ACT CCT AGG TTC GAA CGC CGG 5'
  T   A   G   T   C   Y   *   *
```

pDPH51 Fab 40.4 hinge 1 Δinter IgAtp

```
5'  CT AGT GAC AAA ACT CAC ACC TGC CCG CCG TGC CCG GCG GGC AAA CCG ACC CAT GTG AAC GTG AGC GTG GTG ATG
3'       CA CTG TTT TGA GTG TGG ACG GGC GGC ACG GGC CGC CCG TTT GGC TGG GTA CAC TCG CAC CAC TAC CGC TAC
     T   S   D   K   T   H   T   C   P   P   C   P   A   G   K   P   T   H   V   N   V   S   V   V   M

GCG GAA GTG GAT GGC ACC TGT TAT TGA TGA GGA TCC AAG CTT GC      3'
CGC CTT CAC CTA CCG TGG ACA ATA ACT ACT CCT AGG TTC GAA CGC CGG 5'
  A   E   V   D   G   T   C   Y   *   *
```

Table 1 (continued)

pDPH61 Fab 40.4 'IgG2 like' hinge Δinter

```
5'  CT AGT GAC AAA ACT CAC ACC TGC TGC GTG GAA TGC CCG CCG TGC CCG GCG TGA TGA GGA TCC AAG CTT GC      3'
3'       A CTG TTT TGA GTG TGG ACG ACG CAC CTT ACG GGC GGC ACG GGC CGC ACT ACT CCT AGG TTC GAA CGC CGG 5'
    T   S   D   K   T   H   T   C   C   V   E   C   P   P   C   P   A   *   *
```

pDPH62 Fab 40.4 'IgG3' like' hinge Δinter

```
5'  CT AGT GAC AAA ACT CAC ACC TGC CCG CGT TGC CCG GAA CCG AAA AGC TGC GAT ACC CCG CCG CCG TGC CCG CGT TGC CCG GCG
3'       A CTG TTT TGA GTG TGG ACG GGC GCA ACG GGC CTT GGC TTT TCG ACG CTA TGG GGC GGC GGC ACG GGC GCA ACG GGC CGC
    T   S   D   K   T   H   T   C   P   R   C   P   E   P   K   S   C   D   T   P   P   P   C   P   R   C   P   A

TGA TGA GGA TCC AAG CTT GC      3'
ACT ACT CCT AGG TTC GAA CGC CGG 5'
  *   *
```

pDPH63 Fab 40.4 'IgG4 like' hinge Δinter

```
5'  CT  AGT GAC AAA ACT CAC ACC TGC CCG AGC TGC CCG GCG TGA TGA GGA TCC AAG CTT GC      3'
3'       A CTG TTT TGA GTG TGG ACG GGC TCG ACG GGC CGC ACT ACT CCT AGG TTC GAA CGC CGG 5'
    T   S   D   K   T   H   T   C   P   S   C   P   A   *   *
```

Table II

Effect of hinge sequences on efficiency of di-Fab formation *in vivo* in shake flask experiments.

		% di-HC
A5B7 Δinter, hinge ½	TSDKTHTCAA	Non det.
A5B7 Δinter, hinge 1	TSDKTHTCPPCPA	7.375 ± 2.338
A5B7 Δinter, hinge 2o	TSDKTHTCPPCPATCPPCPA	4.804 ± 3.23
A5B7 Δinter, hinge 2i	TSDKTHTCPPCPAGTCPPCPA	Non det.
A5B7 Δinter, hinge 2ii	TSDKTHTCPPCPAGGTCPPCPA	Non det.
A5B7 Δinter, hinge 2iii	TSDKTHTCPPCPAGGGTCPPCPA	Non det.
A5B7 Δinter, hinge 2iv	TSDKTHTCPPCPAGGGGTCPPCPA	Non det.
A5B7 Δinter, hinge 2v	TSDKTHTCPPCPAKGKGETCPPCPA	Non det.
Fab 40.4 Δinter, hinge ½	TSDKTHTCAA	Non det.
Fab 40.4 Δinter, hinge 1	TSDKTHTCPPCPA	35.7 ± 4.85
Fab 40.4 Δinter, hinge 2o	TSDKTHTCPPCPATCPPCPA	25.1 ± 8.43
Fab 40.4 Δinter, hinge 3o	TSDKTHTCPPCPATCPPCPATCPPCPA	20.8 ± 3.58
Fab 40.4 Δinter, hinge 2_{-1}	TSDKTHTCPPCPTCPPCPA	8.1+ ± 4.3
Fab 40.4 Δinter, hinge 2_{-2}	TSDKTHTCPPCPCPPCPA	49.8 ± 16.78
Fab 40.4 hinge 1 + Cys	TCDKTHTCPPCPA	14.4 ± 9.75
Fab 40.4 hinge 2o + Cys	TCDKTHTCPPCPATCPPCPA	16.3 ± 2.30
Fab 40.4 'IgG2 like' hinge Δinter	TSDKTHTCCVECPPCPA	20.8 ± 5.95
Fab 40.4 'IgG3' like' hinge Δinter	TSDKTHTCPRCPEPKSCDTPPPCPRCPA	29.3 ± 5.95
Fab 40.4 'IgG4 like' hinge Δinter	TSDKTHTCPSCPA	8.63 ± 1.41

Table III

Effect of hinge composition on $F(ab')_2$ pharmacokinetics in rat.

	No. hinge disulphides	AUC (% id.hr)	SEM (% id.hr)	t½α (hr)	SEM (hr)	t½β (hr)	SEM (hr)	n
Fab 40.4 $F(ab')_2$ 'hinge ½'	1	166.2	9.8	1.3	0.04	19.0	1.8	6
Fab 40.4 $F(ab')_2$ 'hinge 1'	≤ 2	423.6	35.0	2.1	0.1	13.1	0.2	6
Fab 40.4 $F(ab')_2$ 'hinge 2o'	≤ 4	509.7	31.4	3.0	0.2	11.0	0.5	10
Fab 40.4 DFM	1 thioether	384.2	32.1	2.3	0.1	16.4	0.3	6

FIGURE LEGENDS

Figure 1. Effect of hinge sequence and complexity of di-Fab' formation *in vivo.*
Anti-Fd western blot of 4-20% Tris-glycine SDS-PAGE, reducing for lanes 1 and 2, non-reducing for lanes 3 to 12. Molecular size of standards (kDa) are shown on the right. All periplasmic samples loaded equally, except LC only control (lane 4) which has a 5 fold excess. Lane 1, pDPH52 Fab 40.4 hinge 1 + cys; lane 2, pDPH44 Fab 40.4 hinge 1 inter; lane 3, purified Fab' 40.4 + cys control; lane 4, Fab 40.4 light chain only control; lane 5, pDPH42 Fab 40.4 hinge 2o + cys; lane 6, pDPH52 Fab 40.4 hinge 1 + cys; lane 7, pDPH54 Fab 40.4 hinge 2_{-2} inter; lane 8, pDPH53 Fab 40.4 hinge 2_{-1} inter; lane 9, pDPH69 Fab 40.4 hinge 3o inter; lane 10, pDPH41 hinge 2o inter; lane 11, pDPH44 hinge 1 inter; lane 12, pDPH40 hinge inter.

Figure 2. Comparison of effect of hinge isotype on di-Fab' formation *in vivo.*
Anti-Fd western blot of 4-20% Tris-glycine non-reducing SDS-PAGE. Molecular size of standards (kDa) are shown on the right. All periplasmic samples loaded equally, except LC only control (lane 1) which has a 5 fold excess. Lane 1, Fab 40.4 light chain only control; lane 2, purified Fab' 40.4 + cys control; lane 3, pDPH63 Fab 40.4 'IgG4 like' hinge inter; lane 4, pDPH62 Fab 40.4 'IgG3 like' hinge inter; lane 5, pDPH62 Fab 40.4 'IgG2 like' hinge inter; lane 6, pDPH44 Fab 40.4 hinge 1 inter (IgG1).

Figure 3. Effect of hinge sequences and duration of oxidation on $F(ab')_2$ formation *in vitro*.
The mean and SD of three independent experiments conduction at pH 8.0 and room temperature are shown.

Figure 4. Range of $F(Ab')_2$ molecules capable of being formed
A. $F(ab')_2$ formed by 'hinge 1', and **B**, $F(ab')_2$ formed by 'hinge 2o', only the 'head to head' forms are shown for 'hinge 2o', hence the use of 'x2' to denote possible 'head to tail' forms.

Figure 5. Effect of hinge sequence on resistance of $F(ab')_2$ to reduction *in vitro*
$F(Ab')_2$ at 0.25mgml^{-1} are subjected to reduction at pH 7.0, 37°C for 45 min. at the range of b-MA concentrations shown.

Figure 6. Effect of hinge composition on $F(ab')_2$ pharmacokinetics in rat.
The mean and standard error of mean for each $F(ab')_2$ are shown. T here were six animals in each group, except 'hinge 2o' where n=10.

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CLAIMS

1. A peptide of Formula (1)

$$^{N}TCPPCPXYCPPCPA^{C} \quad (1)$$

wherein X and Y, which may be the same or different, is each a neutral aliphatic L-amine acid residue, and protected and reactive derivatives thereof.

2. A peptide according to Claim 1 wherein X is an alanine residue.

3. A peptide according to Claim 1 or Claim 2 wherein Y is a threonine residue.

4. A protein comprising one polypeptide chain characterised in that said chain contains an amino acid sequence $^{N}TCPPCPXYCPPCPA^{C}$ wherein X and Y are as defined in Claim 1.

5. A protein comprising two polypeptide chains characterised in that each of said chains contains an amino acid sequence $^{N}TCPPCPXYCPPCPA^{C}$ wherein X and Y are as defined in Claim 1 and each chain is covalently linked to the other through one, two, three or four of the cysteine residues present in each of said amino acid sequences.

6. A protein according to Claim 4 or Claim 5 which is an antibody or an antigen binding fragment thereof.

7. A protein according to Claim 6 which is a Fab or Fab' fragment.

8. A protein according to any one of Claim 4 to Claim 7 which has one or more effector or reporter molecules attached to it.

FIG. 1

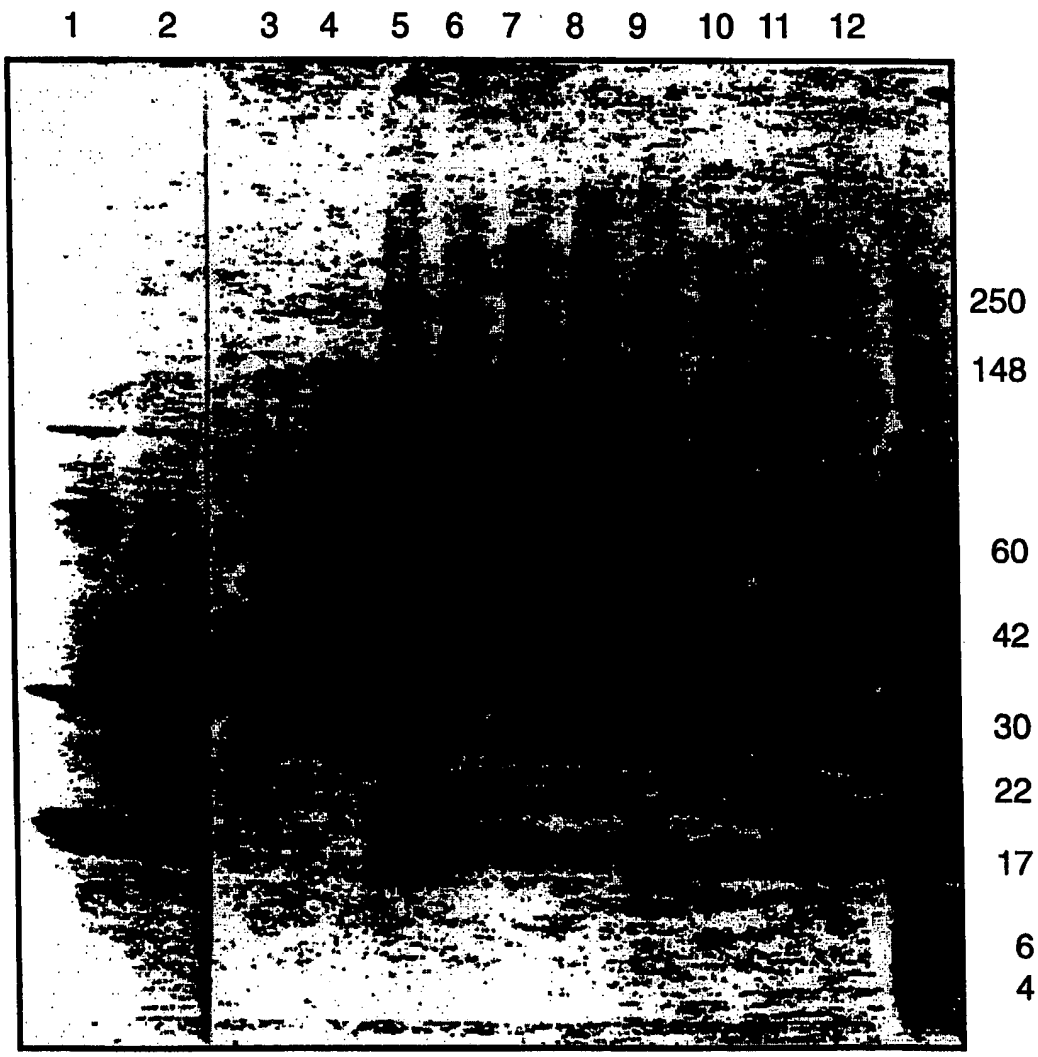


FIG. 2

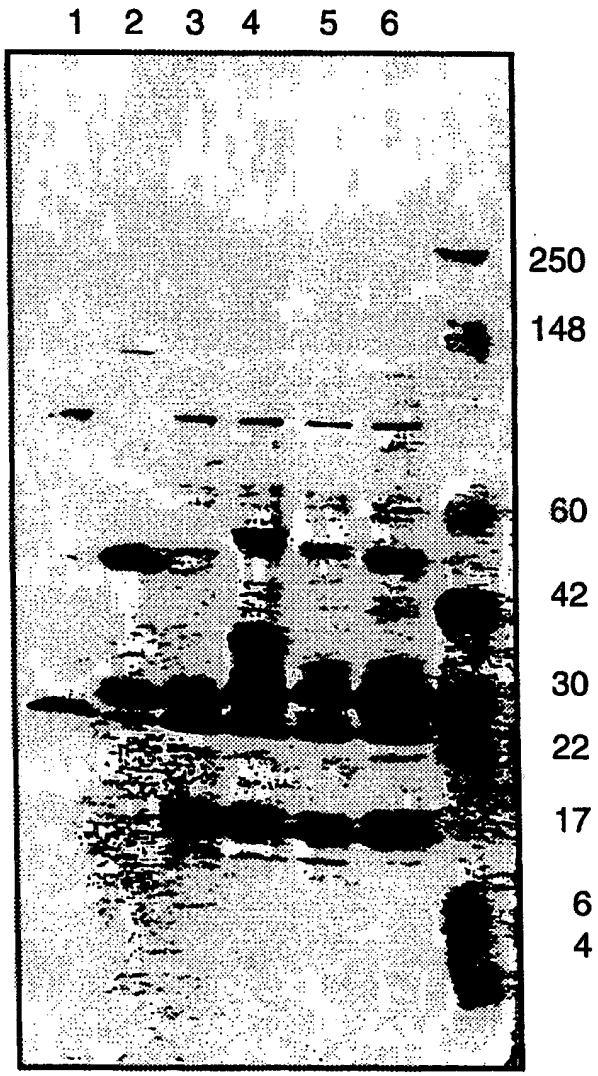
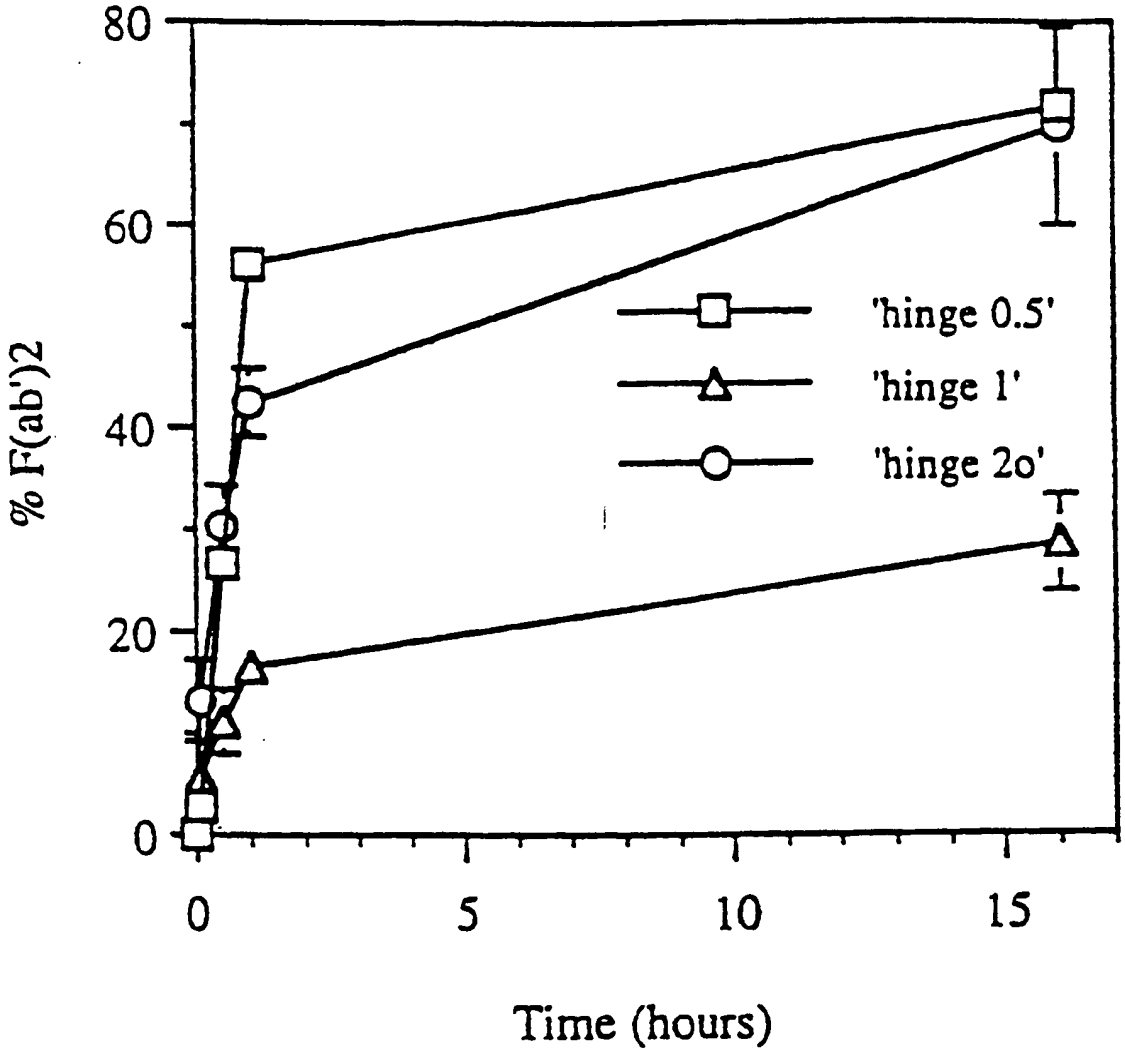


FIG. 3



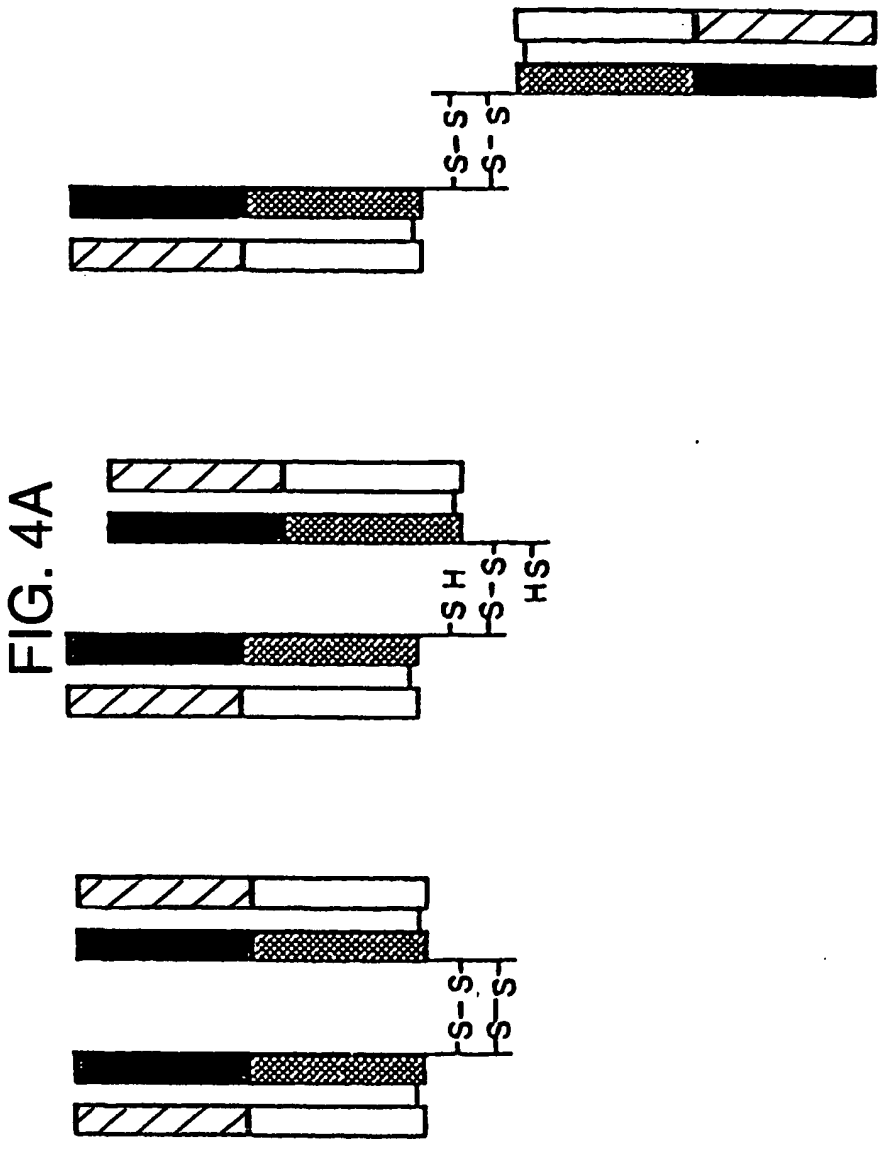


FIG. 4A

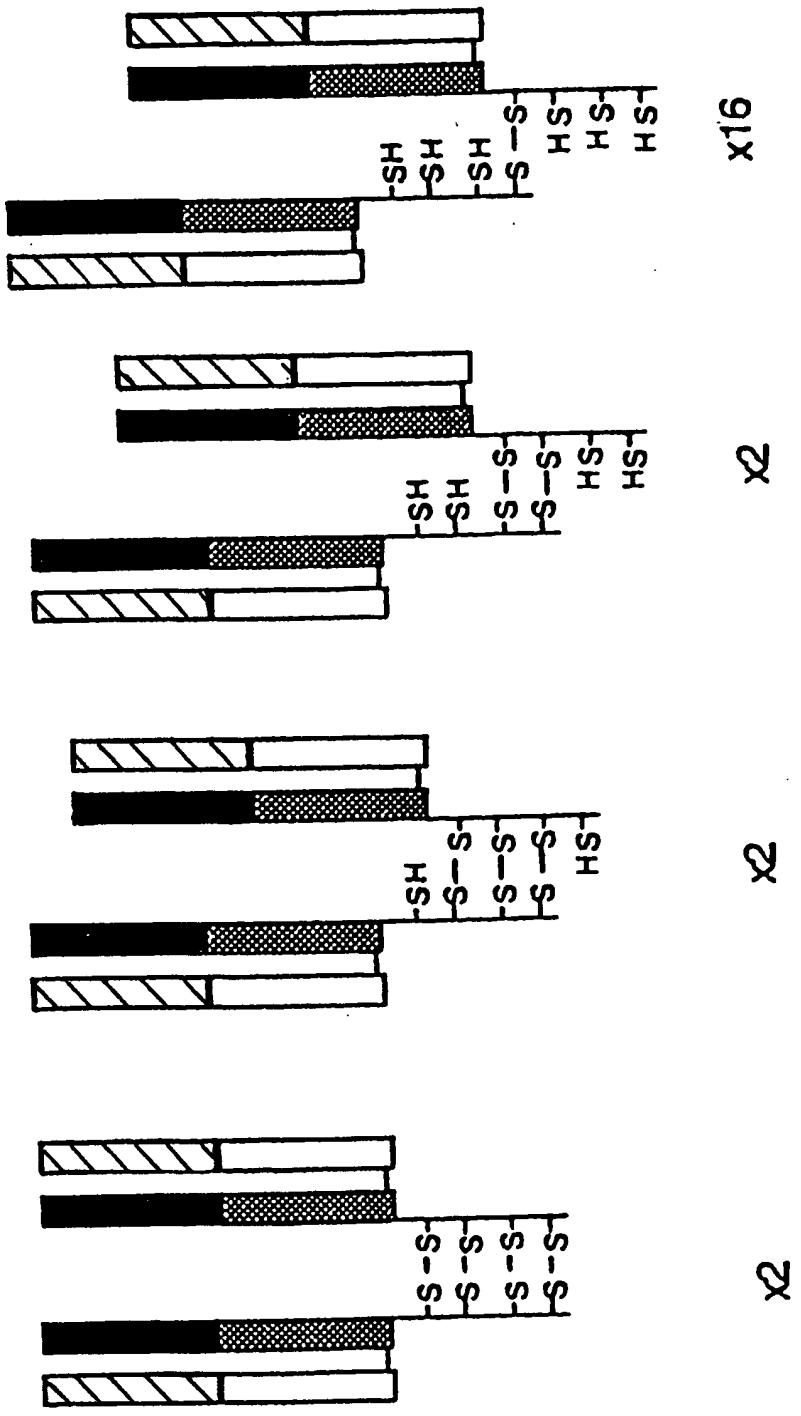


FIG. 4B

FIG. 5

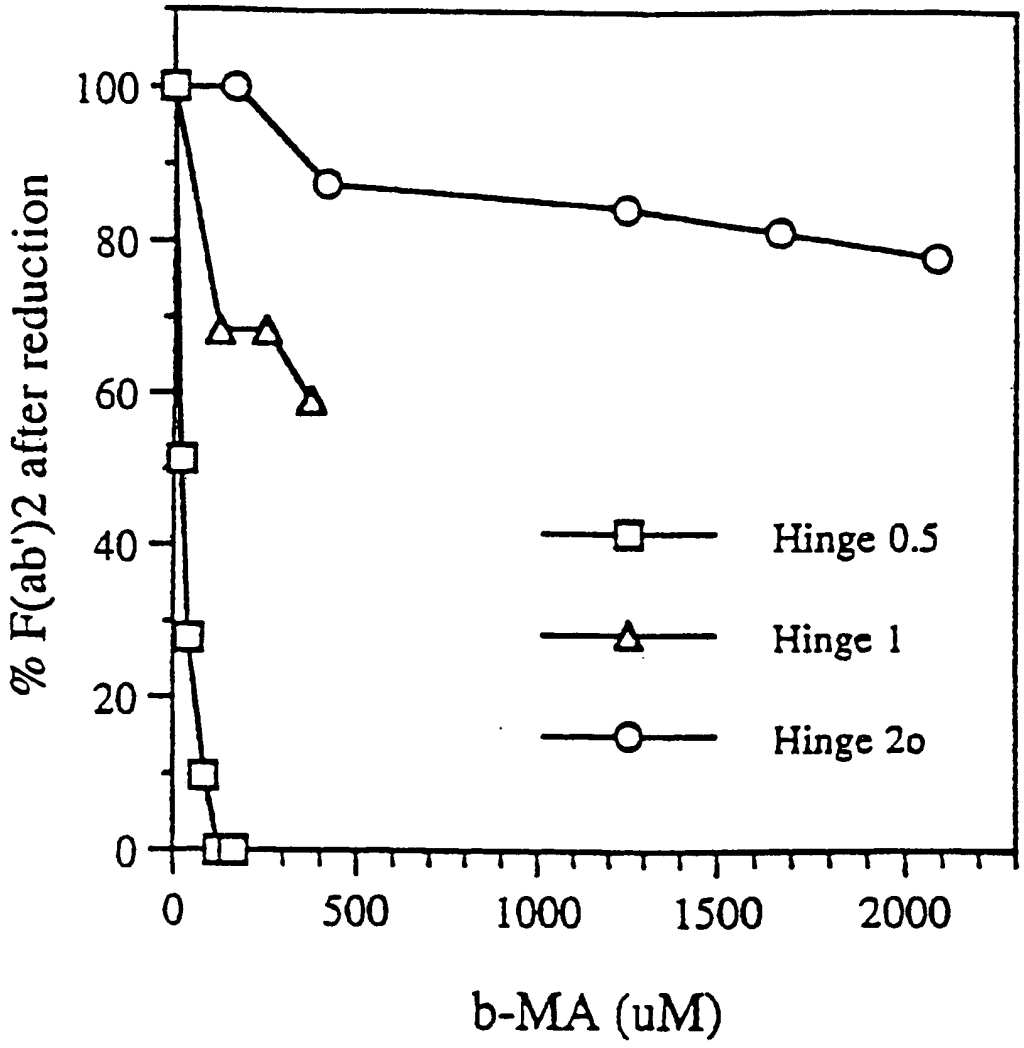
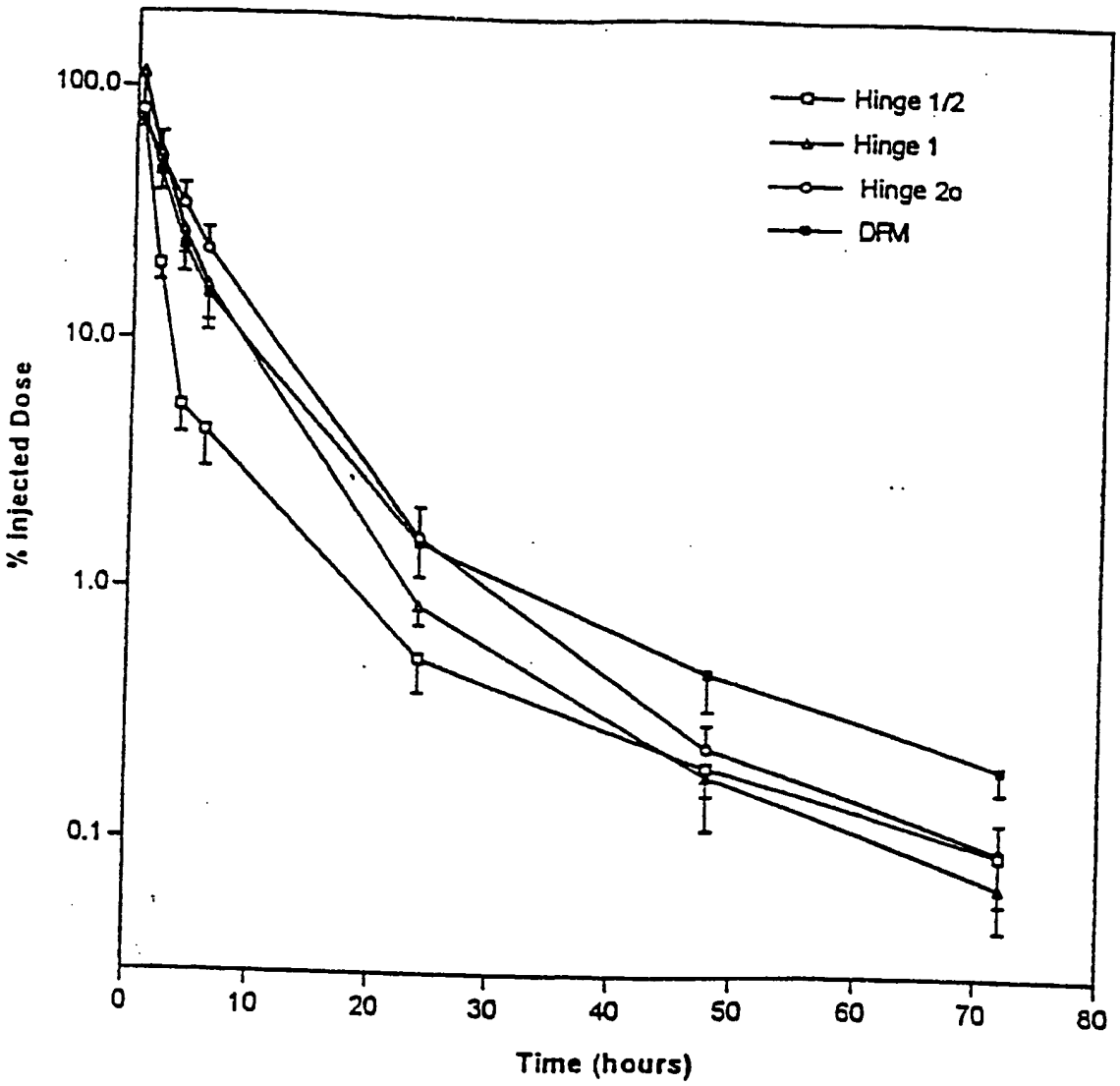

% F(ab')2 after reduction
100
80
60
40
20
0
0
500
1000
1500
2000
b-MA (uM)
Hinge 0.5
Hinge 1
Hinge 2o

FIG. 6


100.0
10.0
1.0
0.1
% Injected Dose
0
10
20
30
40
50
60
70
80
Time (hours)
Hinge 1/2
Hinge 1
Hinge 2o
DRM